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RAW SEQUENCE LISTING

DATE: 10/17/2001

PATENT APPLICATION: US/09/924,338

TIME: 15:39:53

Input Set : N:\Crf3\RULE60\09924338.txt

Output Set: N:\CRF3\10172001\I924338.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

- 6 (i) APPLICANT: Tobin, James
- 8 (ii) TITLE OF INVENTION: HUMAN INTERLEUKIN-11 RECEPTOR
- 10 (iii) NUMBER OF SEQUENCES: 4
- 12 (iv) CORRESPONDENCE ADDRESS:
 - 13 (A) ADDRESSEE: Genetics Institute, Inc.
 - 14 (B) STREET: 87 CambridgePark Drive
 - 15 (C) CITY: Cambridge
 - 16 (D) STATE: MA
 - 17 (E) COUNTRY: USA
 - 18 (F) ZIP: 02140

ENTERED

20 (v) COMPUTER READABLE FORM:

- 21 (A) MEDIUM TYPE: Floppy disk
- 22 (B) COMPUTER: IBM PC compatible
- 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

26 (vi) CURRENT APPLICATION DATA:

- C--> 27 (A) APPLICATION NUMBER: US/09/924,338
- C--> 28 (B) FILING DATE: 07-Aug-2001
- 29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

- 32 (A) APPLICATION NUMBER: 09/151,102
- 33 (B) FILING DATE: 1998-09-10
- 35 (A) APPLICATION NUMBER: 08/362,304
- 36 (B) FILING DATE: 22-DEC-1994

38 (viii) ATTORNEY/AGENT INFORMATION:

- 39 (A) NAME: Brown, Scott A.
- 40 (B) REGISTRATION NUMBER: 32,724
- 41 (C) REFERENCE/DOCKET NUMBER: GI5252

43 (ix) TELECOMMUNICATION INFORMATION:

- 44 (A) TELEPHONE: (617) 498-8224
- 45 (B) TELEFAX: (617) 876-5851

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

- 51 (A) LENGTH: 2456 base pairs
- 52 (B) TYPE: nucleic acid
- 53 (C) STRANDEDNESS: double
- 54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

58 (iii) HYPOTHETICAL: NO

61 (ix) FEATURE:

- 62 (A) NAME/KEY: CDS
- 63 (B) LOCATION: 734..1999

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

68 TCGCCACCC CCAGCCTCTG GCAGCAGCCA GGGCATCTGG ATCTGCTTAA CTACACAGCC 60
 70 CCAGCCTGCA CCCTAGCCCC ATCCAGCTTC ACAAAGTGA GACCAACGAA GTGTCAAGAG 120

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72 CCAGGCCCAG CTGAGTGGCC CAAGTAGCCA GACCAAGGAG CCAGGTTTCAG GCGAGAAGCC 180
74 TGGCAGCCAG GGCAGGGGTG GGCCTCAGGG TGGGAGTGCA GGATGGGCTC AGATCCATGA 240
76 TGACACCCTT CCCCCAGGGT GATAAGGTCT GCCTAGGTTA ATCAGAGGCA GTGATAAGCC 300
78 CTGGACCAGG TGGGGGTAAA TACCAGAATT CCCAACAGCT GGAAGTGGAGG GGTAAATGGG 360
80 AGTGGCTGAG CTGGTGCCAG TGCTTGCTGC CAGGGGTGGG CGCCAAGGGC AGTGGAGGGG 420
82 GAGTTGCTGG CACAGTCTGT TGCCTCCGGC TTTTGTTCTG GGCCCTAAGC CCAGGACTGA 480
84 GATGGAGGGT GTGAGGGGGT GTGTGTGTCC GTGTGTGTGT GTGTGTGTGT GTGCGCGCGC 540
86 ACGCACATGC AAAGCACTGG GTATACAGTG GGAAAGGGGA CCTCAGGTCA GTTCCCCGAG 600
88 TGATTCTAA CAGCCTTACC CCACTTGGTG CATCAATTTT TCTCCTAGGA AGCCTCAGTT 660
90 TTGGAGAGGA AGAGCCAGGC TTTAGCCTCC CATCTCAGGG GTCGGGGATT TTTGACTCTA 720
92 CCTCTCCCCA CAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG 769
93 Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu
94 1 5 10
96 GTG GCC GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG 817
97 Val Ala Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln
98 15 20 25
100 GCC TGG GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG 865
101 Ala Trp Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val
102 30 35 40
104 AAG CTG TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT 913
105 Lys Leu Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe
106 45 50 55 60
108 CGG GAT GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG 961
109 Arg Asp Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly
110 65 70 75
113 CAT GAA CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC 1009
114 His Glu Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr
115 80 85 90
117 ATC TGC CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG 1057
118 Ile Cys Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln
119 95 100 105
121 CTG GGC TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC 1105
122 Leu Gly Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp
123 110 115 120
125 TAT GAG AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA 1153
126 Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu
127 125 130 135 140
129 CCC ACC CGC TAC CTC ACC TCC TAC AGG AAG AAG ACA GTC CTA GGA GCT 1201
130 Pro Thr Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala
131 145 150 155
133 GAT AGC CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG 1249
134 Asp Ser Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln
135 160 165 170
137 GAT CCC CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG 1297
138 Asp Pro Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp
139 175 180 185
141 AGC CAG TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GCC AGC 1345
142 Ser Gln Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser
143 190 195 200

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145	ACA CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA	1393
146	Thr Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro	
147	205 210 215 220	
149	CCC CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA CGC CTG	1441
150	Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu	
151	225 230 235	
153	CGA GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC	1489
154	Arg Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe	
155	240 245 250	
157	CTG CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG	1537
158	Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp	
159	255 260 265	
161	TCC ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG	1585
162	Ser Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val	
163	270 275 280	
165	GCT GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT	1633
166	Ala Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp	
167	285 290 295 300	
169	GCT GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC	1681
170	Ala Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser	
171	305 310 315	
173	ACT GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG	1729
174	Thr Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr	
175	320 325 330	
177	CAG CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC	1777
178	Gln Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro	
179	335 340 345	
181	TCC CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG	1825
182	Ser Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu	
183	350 355 360	
185	CAG GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG	1873
186	Gln Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu	
187	365 370 375 380	
189	GTG GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT	1921
190	Val Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly	
191	385 390 395	
193	GGG AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA	1969
194	Gly Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro	
195	400 405 410	
197	GTG GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT	2019
198	Val Asp Arg Arg Pro Gly Ala Pro Asn Leu	
199	415 420	
201	CGGCAGATTC CACCTATAAT TCTGTCTTGC TGGTGTGGAT GGATGGACAG ATAGAAACCA	2079
203	GGCAGGACAG TAGATCCCTA TGGTTGGATC TCAGCTGGAA GTTCTGTTT GAGCCCATTT	2139
205	CTGTGAGACC CTGTATTTCA AATTTCAGC TGAAAGGTGC TTGTACCTCT GATTTCACCC	2199
207	CAGAGTTGGA GTTCTGCTCA AGGAACGTGT GTAATGTGTA CATCTGTGTC CATGTGTGAC	2259
209	CATGTGTCTG TGAGGCAGGG AACATGTATT CTCTGCATGC ATGTATGTAG GTGCCTGGGG	2319
211	AGTGTGTGTG GGTCCCTGGC TCTTGGCCTT TCCCTTGCA GGGGTTGTGC AGGTGTGAAT	2379
213	AAAGAGAATA AGGAAGTTCT TGGAGATTAT ACTCAGAAAA AAAAAAAAAA AGTCGACGCG	2439

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215 GCCGCGAATT CCTGCAG 2456

219 (2) INFORMATION FOR SEQ ID NO: 2:

221 (i) SEQUENCE CHARACTERISTICS:

222 (A) LENGTH: 422 amino acids

223 (B) TYPE: amino acid

224 (D) TOPOLOGY: linear

226 (ii) MOLECULE TYPE: protein

228 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

230 Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala

231 1 5 10 15

233 Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro

234 20 25 30

236 Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu Cys Cys

237 35 40 45

239 Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp Gly Glu

240 50 55 60

242 Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu Leu Val

243 65 70 75 80

245 Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys Gln Thr

246 85 90 95

248 Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly Tyr Pro

249 100 105 110

251 Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe

252 115 120 125

254 Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr

255 130 135 140

257 Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser Gln Arg

258 145 150 155 160

260 Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly

261 165 170 175

263 Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg

264 180 185 190

266 Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Arg Leu Leu

267 195 200 205

269 Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu

270 210 215 220

272 Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu Arg Ala Ser Trp

273 225 230 235 240

275 Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys Phe

276 245 250 255

278 Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu

279 260 265 270

281 Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro

282 275 280 285

284 His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp

285 290 295 300

287 Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr Ile

288 305 310 315 320

290 Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu Val

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291          325          330          335
293 Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser Leu Gln Pro
294          340          345          350
296 His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln Val Ala Val
297          355          360          365
299 Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val Ala Gly Ala
300          370          375          380
302 Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly Lys Asp Gly
303 385          390          395          400
305 Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val Asp Arg Arg
306          405          410          415
308 Pro Gly Ala Pro Asn Leu
309          420
312 (2) INFORMATION FOR SEQ ID NO: 3:
314 (i) SEQUENCE CHARACTERISTICS:
315 (A) LENGTH: 1714 base pairs
316 (B) TYPE: nucleic acid
317 (C) STRANDEDNESS: double
318 (D) TOPOLOGY: linear
320 (ii) MOLECULE TYPE: cDNA
322 (iii) HYPOTHETICAL: NO
325 (ix) FEATURE:
326 (A) NAME/KEY: CDS
327 (B) LOCATION: 34..1359
330 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
332 TTCTTAGCCT GATAGGAGGA AGTCTTGAG GCC ATG GCA CTC AGT CAC TGT GAT      54
333          Met Ala Leu Ser His Cys Asp
334          1          5
336 TAT CAA GAT GAG CAG CAG CTG CTC AGG GCT GAC CAG GGT CCT GGT GGC      102
337 Tyr Gln Asp Glu Gln Gln Leu Leu Arg Ala Asp Gln Gly Pro Gly Gly
338          10          15          20
340 CGT GCT ACA GCC CTG GTG TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG      150
341 Arg Ala Thr Ala Leu Val Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp
342          25          30          35
344 GGT CCT CCA GGG GTC CAG TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG      198
345 Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu
346 40          45          50          55
348 TGC TGC CCC GGA GTG AGT GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT      246
349 Cys Cys Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp
350          60          65          70
352 GGA GAT TCA AGG CTG CTC CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA      294
353 Gly Asp Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg
354          75          80          85
356 CTG GTC TTG GCC CAG GTG GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC      342
357 Leu Val Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys
358          90          95          100
360 CAG ACC CTG GAT GGT GTA TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC      390
361 Gln Thr Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly
362          105          110          115

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VERIFICATION SUMMARY

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TIME: 15:39:54

Input Set : N:\Crf3\RULE60\09924338.txt

Output Set: N:\CRF3\10172001\I924338.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]